IN THE UNITED STATES PATENT AND TRADEMARK OFFICE	Application Number	**10/073,054**
	Filing Date	**February 12, 2002**
	First Named Inventor	**HERZOG**
	Group Art Unit	**1632**
	Examiner Name	**Shukla, Ram R.**
	Attorney Docket Number	**1871-132**

Title: **NOVEL G PROTEIN-COUPLED RECEPTOR AND DIAGNOSTIC USES THEREFOR**

RESPONSE TO RESTRICTION REQUIREMENT

Commissioner for Patents
United States Patent and Trademark Office
P.O. Box 1450
Alexandria, Virginia 22313-1540

Dear Sir:

In an Office Action dated September 9, 2004, the period for responding to which has been extended by two months, the examiner asserted that applicants' response filed on June 16, 2004 is not fully responsive to the restriction requirement in the Office Action of January 16, 2004. According to the Examiner, paragraph 3 of that Office Action required the election of a SEQ ID No, which election was not made. Therefore, the Examiner asserts applicants have not elected an invention nor made an election of species as required.

In the Office Action of January 16, 2004 the Examiner asserted that the above-referenced patent application contains more than one invention and requested that the Applicants elect one of the following inventions for initial prosecution on the merits:

Group I, claims 1-11, 16, 17, 19, drawn to a GPR56 polynucleotide and a gene construct comprising the polynucleotide.

Group II, claims 11-14, drawn to a GPR56 polypeptide.

Group III, claim 15, drawn to an antibody to a GPR56 polypeptide.

Group IV, claims 18 and 20, drawn to a GPR56 probe comprising the sequence of a certain SEQ ID No.

Group V, claims 21-41, drawn to a diagnostic method of determining the level of GPR56 mRNA in a test sample.

Group VI, claims 42-46, drawn to a method for detecting a cancer cell in a subject by determining the level of a GPR56 polypeptide.

In applicants' response of June 16, 2004, the claims of Group V, i.e. claims 21-41, were elected for initial prosecution on the merits. Applicants further elect with traverse the sequence set forth in SEQ ID No:14.

Applicants traverse the election of a single SEQ ID No because there is no undue burden imposed on the Examiner in searching all of the sequences referenced in claims 21-41. These claims reference SEQ ID No:1 and each of SEQ ID Nos:11-19. Each of the SEQ ID Nos:11-19 is derived from the full length sequence set forth in SEQ ID No:1 or the complementary sequence thereto. Each of these sequences (SEQ ID Nos:11-19) satisfies the structural requirements set forth in the description at page 59, lines 4-21, of the specification. Therefore, the nucleotide sequences in claims 21-41 are broadly related in structure, either as SEQ ID No:1 or being derived from SEQ ID No:1 or its complementary sequence.

In addition to the broad structural similarity between all of SEQ ID Nos:11-19, there is considerable sequence identity among the sequences. Applicants submit that SEQ ID No:14 and

SEQ ID No:11 are related to each other as reverse complementary sequences derived from nucleotides 327 to 348 of SEQ ID No:1. Further, SEQ ID No:15 and SEQ ID No:12 are similarly related to each other, being derived from nucleotides 1383 to 1404 of SEQ ID No:1. Similarly, SEQ ID No:16 and SEQ ID No:13 are related to each other as reverse complementary sequences derived from nucleotides 940 to 962 of SEQ ID No:1. Further, SEQ ID Nos:17 and 18 are overlapping sequences that share a 16 nucleotide overlap in a region complementary to nucleotides 1662 to about 1686 of SEQ ID No:1. Further, SEQ ID No:19 encompasses each of SEQ ID Nos:17 and 18 with only a single nucleotide mismatch in the overlapping regions. Therefore, applicants submit that a standard BLAST search for each of SEQ ID Nos:14-17 will identify references disclosing any SEQ ID Nos:11-19. A search for SEQ ID Nos:14-16 will also identify references relating to their complementary sequences SEQ ID Nos:11-13, and a search for SEQ ID No:17 will also identify references relating to SEQ ID Nos:18-19 because SEQ ID Nos:17-19 share an overlapping sequence. For these reasons, applicants submit that examination of a reasonable number of sequences, namely four sequences, i.e. SEQ ID Nos:14-17, would cover examination of SEQ ID Nos:11-19 in the present application.

Furthermore, applicants submit that the Official Gazette of November 19, 1996, in the section "Examination of Patent Applications Containing Nucleotide Sequences", states that the USPTO will permit applications to claim up to ten (10) independent and distinct nucleotide sequences in one national application. Moreover, the notice also states that; "Nevertheless, to further aid the biotechnology industry in protecting its intellectual property without creating an undue burden on the Office, the Commissioner has decided *sua sponte* to partially waive the

requirements of 37 CFR 1.141 et seq. and permit a reasonable number of such nucleotide sequences to be claimed in a single application." Further, "accordingly, and in most cases, up to ten (10) independent and distinct nucleotide sequences will be examined in a single application without restriction. It has been determined that normally ten (10) sequences constitute a reasonable number for examination purposes."

Therefore, applicants respectfully submit that the presently elected invention in Group V, i.e. claims 21-41 without electing a single sequence does not impose an undue burden on the Examiner for examination. In case the Examiner maintains that an election of a single SEQ ID No is required applicants elect SEQ ID No:14 for initial prosecution on the merits. With such election of SEQ ID No:14 applicants further request a rejoinder of SEQ ID No:11 because any BLAST search for SEQ ID No:14 will necessarily identify SEQ ID No:11. Therefore, there is no undue burden on the Examiner in conducting a search of at least both of these sequences.

Applicants respectfully submit that the application is in condition for allowance. Consideration and favorable action are earnestly requested.

RESPECTFULLY SUBMITTED,					
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